OIPE

RAW SEQUENCE LISTINGPATENT APPLICATION: US/09/754,947

DATE: 07/02/2001

TIME: 16:41:09

Input Set : A:\-33-1.app

Output Set: N:\CRF3\07022001\I754947.raw

ENTERED

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3 <110> APPLICANT: Lee, Bruce Andrew
         Flores, Becky Mar
 5
         Valkirs, Gunars Edwin
        Biosite Diagnostics, Inc.
 8 <120> TITLE OF INVENTION: Assays for Detection of Bacillus Anthracis
10 <130> FILE REFERENCE: 014907-003310US
12 <140> CURRENT APPLICATION NUMBER: US 09/754,947
13 <141> CURRENT FILING DATE: 2001-01-04
15 <150> PRIOR APPLICATION NUMBER: US 60/174,901
16 <151> PRIOR FILING DATE: 2000-01-06
18 <160> NUMBER OF SEQ ID NOS: 5
20 <170> SOFTWARE: PatentIn Ver. 2.1
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 785
24 <212> TYPE: PRT
25 <213> ORGANISM: Bacillus anthracis
27 <220> FEATURE:
28 <223> OTHER INFORMATION: surface array protein (SAP)
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40 Met Met Ala Gln Ile Leu Asn Leu Pro Ile Asp Lys Asp Ala Lys Pro
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43 Ser Phe Ala Asp Ser Gln Gly Gln Trp Tyr Thr Pro Phe Ile Ala Ala
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46 Val Glu Lys Ala Gly Val Ile Lys Gly Thr Gly Asn Gly Phe Glu Pro
49 Asn Gly Lys Ile Asp Arg Val Ser Met Ala Ser Leu Leu Val Glu Ala
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52 Tyr Lys Leu Asp Thr Lys Val Asn Gly Thr Pro Ala Thr Lys Phe Lys
                              120
55 Asp Leu Glu Thr Leu Asn Trp Gly Lys Glu Lys Ala Asn Ile Leu Val
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58 Glu Leu Gly Ile Ser Val Gly Thr Gly Asp Gln Trp Glu Pro Lys Lys
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61 Thr Val Thr Lys Ala Glu Ala Ala Gln Phe Ile Ala Lys Thr Asp Lys
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64 Gln Phe Gly Thr Glu Ala Ala Lys Val Glu Ser Ala Lys Ala Val Thr
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                         67 Thr Gln Lys Val Glu Val Lys Phe Ser Lys Ala Val Glu Lys Leu Thr
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70 Lys Glu Asp Ile Lys Val Thr Asn Lys Ala Asn Asn Asp Lys Val Leu
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		Tyr	Ser	Asn	Leu 245		Ala	Lys	Gln	Thr 250		Thr	Val	Asp	Val 255	
	Lys	Val	Gly	Lys 260		Glu	Val	Ala	Val 265		Ser	Leu	Glu	Ala 270		Thr
	Ile	Glu	Met 275		Asp	Gln	Thr	Val 280		Ala	Asp	Glu	Pro 285		Ala	Leu
	Gln	Phe 290	Thr	Val	Lys	Asp	Glu 295		Gly	Thr	Glu	Val 300	_	Ser	Pro	Glu
	_		Glu	Phe	Val	Thr 310		Ala	Ala	Glu	Lys 315		Asn	Ala	Lys	Gly 320
	-	Ile	Thr	Leu	Ala 325		Gly	Thr	Ser	Thr 330		Val	Lys	Ala	Val 335	
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97 <i>i</i> 98	Ala	Glu	Gly 355	Ala	Ala	Val	Ala	Ser 360	Ile	Ser	Asn	Trp	Thr 365	Val	Ala	Glu
100 101		Asr 370		: Ala	Asp	Phe	Thr 375		Lys	s Asp	Phe	2 Lys		Asr	a Asr	Lys '
	Val	_	Glu	Gly	Asp	Asn 390		туг	· Val	L Glr	val 395		Leu	Lys	a Asp	Gln 400
106 107		. Asn	a Ala	val	. Thr 405		Gly	Lys	val	410		Glu	ser	Leu	Asr 415	Thr
109 110	Glu	Val	Ala	Val 420		Asp	Lys	. Alā	Thr 425		, Lys	Val	Thr	Val 430		ser
112 113		Gly	Lys 435		Pro	Val	Lys	Val		val	Lys	a Asp	Ser 445		Gl _y	y Lys
115 116		Leu 450		. Ser	His	Thr	Val 455		ı Ile	e Glu	ı Ala	Phe 460		Glr	Lys	s Ala
	Met 465		: Asp) Ile	. Lys	Leu 470		Lys	Thr	Asr	val 475		Leu	Ser	Thi	Lys 480
121 122	Asp	Val	. Thr	Asp	Leu 485	_	Val	Lys	s Ala	Pro 490		. Leu	Asp	Glr	1 Tyr 495	Gly
124 125	Lys	Glu	Phe	Thr 500		Pro	Val	. Thr	Val 505	_	val	. Leu	Asp	510		Gly
127 128	_	Glu	Leu 515	_	Glu	Gln	Lys	520		ı Ala	Lys	Туг	Val 525		Arg	, Glu
	Leu		Leu				_		Glu		_		Туг		· Val	. Val
	Leu 545		Ala	Lys	Ser	Gly 550		Lys	Glu	ı Ala	Lys 555		Thr	Leu	Ala	Leu 560
137			_		565					570)				575	
139 140	Asp	Thr	Glu	Leu 580		Lys	Tyr	Val	. Thr 585		Glu	Asn	Gln	Lys 590		Ala
142 143		Thr	Val 595		Val	Leu	Pro	Val		Ala	Asn	Gly	Leu 605		Leu	Lys
		Ala	Glu	Ala	Ala	Glu	Leu	Lys	Val	. Thr	Thr	Thr	Asn	Lys	Glu	Gly

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151 Val Ile Thr Val Gly Gln Gly Ala Lys Ala Gly Glu Thr Tyr Lys Val
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154 Thr Val Val Leu Asp Gly Lys Leu Ile Thr Thr His Ser Phe Lys Val
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157 Val Asp Thr Ala Pro Thr Ala Lys Gly Leu Ala Val Glu Phe Thr Ser
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160 Thr Ser Leu Lys Glu Val Ala Pro Asn Ala Asp Leu Lys Ala Ala Leu
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163 Leu Asn Ile Leu Ser Val Asp Gly Val Pro Ala Thr Thr Ala Lys Ala
164 705
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166 Thr Ala Ser Asn Val Glu Phe Val Ser Ala Asp Thr Asn Val Val Ala
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169 Glu Asn Gly Thr Val Gly Ala Lys Gly Ala Thr Ser Ile Tyr Val Lys
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172 Asn Leu Thr Val Val Lys Asp Gly Lys Glu Gln Lys Val Glu Phe Asp
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179 785
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195 aaagctggcg ttattaaagg tacaggaaac ggctttgagc caaacggaaa aatcgaccgc 300
196 gtttctatgg catctcttct tgtagaagct tacaaattag atactaaagt aaacggtact 360
197 ccagcaacta aattcaaaga tttagaaaca ttaaactggg gtaaagaaaa agctaacatc 420
198 ttagttgaat taggaatctc tgttggtact ggtgatcaat gggagcctaa gaaaactgta 480
199 actaaagcag aagctgctca attcattgct aagactgaca agcagttcgg tacagaagca 540
200 gcaaaagttg aatctgcaaa agctgttaca actcaaaaag tagaagttaa attcagcaaa 600
201 gctgttgaaa aattaactaa agaagatatc aaagtaacta acaaagctaa caacgataaa 660
202 gtactagtta aagaggtaac tttatcagaa gataaaagat ctgctacagt tgaattatat 720
203 agtaacttag cagctaaaca aacttacact gtagatgtaa acaaagttgg taaaacagaa 780
204 gtagctgtag gttctttaga agcaaaaaca atcgaaatgg ctgaccaaac agttgtagct 840
205 gatgagccaa cagcattaca attcacagtt aaagatgaaa acggtactga agttgtttca 900
206 ccagagggta ttgaatttgt aacgccagct gcagaaaaaa ttaatgcaaa aggtgaaatc 960
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208 gtagctgaaa gtaaagaagt aaaagtttct gctgaaggtg ctgcagtagc ttcaatctct 1080
209 aactggacag ttgcagaaca aaataaagct gactttactt ctaaagattt caaacaaaac 1140
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210 aataaagttt acgaaggcga caacgcttac gttcaagtag aattgaaaga tcaatttaac 1200 211 qcaqtaacaa ctggaaaagt tgaatatgag tcgttaaaca cagaagttgc tgtagtagat 1260 212 aaagctactg gtaaagtaac tgtattatct gcaggaaaag caccagtaaa agtaactgta 1320 213 aaagattcaa aaggtaaagc acttgtttca cacacagttg aaattgaagc tttcgctcaa 1380 214 aaagcaatga aagacattaa attagaaaaa actaacgtag cgctttctac aaaagatgta 1440 215 acagatttaa aagtaaaagc tooagtacta gatcaatacg gtaaagagtt tacageteet 1500 216 gtaacagtga aagtacttga taaagatggt aaagaattaa aagaacaaaa attagaagct 1560 217 aaatatgtga acagagaatt agttctgaat gcagcaggtc aagaagctgg taattataca 1620 218 gttgtattaa ctgcaaaatc tggtgaaaaa gaagcaaaag ctacattagc tctagaatta 1680 219 aaagctccag gtgcattctc taaatttgaa gttcgtggtt tagacacaga attagataaa 1740 220 tatgttactg aggaaaacca aaagaatgca atgactgttt cagttcttcc tgtagatgca 1800 221 aatggattag tattaaaagg tgcagaagca gctgaactaa aagtaacaac aacaaacaaa 1860 222 gaaggtaaag aagtagacgc aactgatgca caagttactg tacaaaataa cagtgtaatt 1920 223 actgttggtc aaggtgcaaa agctggtgag acttataaag taacagttgt actagatggt 1980 224 aaattaatca caactcattc attcaaagtt gttgatacag caccaactgc taaaggatta 2040 225 gcagtagaat ttacaagcac atctcttaaa gaagtagctc caaatgctga tttaaaagct 2100 226 gcacttttaa atatcttatc tqttgatggt gtacctgcga ctacagcaaa agcaacagct 2160 227 totaatgtag aatttgttto tgotgacaca aatgttgtag otgaaaatgg tacagttggt 2220 228 gcaaaaggtg caacatctat ctatgtgaaa aacctgacag ttgtaaaaga tggaaaagag 2280 229 caaaaagtag aatttgataa agctgtacaa gttgcagttt ctattaaaga agcaaaacct 2340 230 gcaacaaaac atcaccatca ccatcactaa 2370 233 <210> SEO ID NO: 3 234 <211> LENGTH: 44 235 <212> TYPE: DNA 236 <213> ORGANISM: Artificial Sequence 238 <220> FEATURE: 239 <223> OTHER INFORMATION: Description of Artificial Sequence:5' PCR primer 241 <400> SEQUENCE: 3 242 tegetgeeca accagecatg geograggta aaacatteec agac 44 245 <210> SEQ ID NO: 4 246 <211> LENGTH: 89 247 <212> TYPE: DNA 248 <213> ORGANISM: Artificial Sequence 250 <220> FEATURE: 251 <223> OTHER INFORMATION: Description of Artificial Sequence:3' PCR primer 253 <400> SEQUENCE: 4 254 gtgataaact accqcattaa agcttatcga tgataagctg tcaattagtg atggtgatgg 60 255 tgatgttttg ttgcaggttt tgcttcttt 258 <210> SEQ ID NO: 5 259 <211> LENGTH: 201 260 <212> TYPE: PRT 261 <213> ORGANISM: Artificial Sequence 263 <220> FEATURE: 264 <223> OTHER INFORMATION: Description of Artificial Sequence: flexible linker 266 <220> FEATURE: 267 <221> NAME/KEY: MOD_RES 268 <222> LOCATION: (1)..(97) 269 <223> OTHER INFORMATION: Gly at positions 1-97 may be present or absent 271 <220> FEATURE:

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VERIFICATION SUMMARY

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